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Result
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4296.941 Million cell updates/sec
      042206 arabidopsis
Q9pxt8 hepatitis c
Q9c5r4 arabidopsis
Q8v7g7 tt virus. o
Q42584 arabidopsis
Q9smu8 arabidopsis
Q9smu8 arabidopsis
Q9a0d7 streptococc
Q92114 rickettsia
Q9z891 chlamydia p
Q92898 chlamydia p
Q92898 schizosacch
Q95xn6 ceanorhabdi
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RESULT 1
Q9P2M2
ID Q9P2M2
PRELIMINARY;
AC Q9P2M2;
PT 01-CCT-2000 (TrEMBLrel. 15, C
PT 01-DCCT-2001 (TrEMBLrel. 15, L
DT 01-DEC-2001 (TrEMBLrel. 19, L
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Q95KA0
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Q8ZD48
Q8ZD48
Q8ZB48
Q8Y8M8
Q9Y827
Q9N948
Q9N948
Q9N929
Q9S169
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Q8WUH0
Q9AK93
Q9AFY3
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Q96FC2
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Q93IF7
Q8XSW3
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Q9SQG6
Q9SQB11
Q9SXB11
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Q36296
                Last sequence update)
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Og4275 lactococcus
Og6pc2 homo sapien
Og31f7 propionibac
Og8xsw3 ralstonia s
Ogbwf1 homo sapien
Og5m84 pasteurella
Og5a48 yersinia pe
Og9sm8 anabaena sp
Og9sm8 anabaena sp
Og9sm8 yersinia pe
Og9sm8 trypanosoma
Og9a27 streptomyce
Og9148 trypanosoma
Og9149 drosophila
Og5109 synechococc
Og91b9 arabidopsis
Og91x23 oryza sativ
Og32863 padinomonas
Og8xzy7 ralstonia s
Og96af8 homo sapien
Og9a70 caenorhabdi
Og9a70 caenorhabdi
Og9a88 arabidopsis
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Q9crr7 mus musculu
Q91wp3 mus musculu
Q91wp3 mus musculi
Q9y483 homo sapien
Q9y483 homo sapien
Q9y612 xylella fas
Q99w60 staphylococ
Q9p883 agarricus bi
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Q64784 avian adeno
Q8xp53 clostridium
Q94818 homo sapien
Q9sqg7 lycopersico
Q9sqg6 lycopersico
Q9sqg6 lycopersico
Q82811 arabidopsis
Q99xa3 staphylococ
Q8w071 oryza sativ
Q9h1w6 homo sapien
Q8r562 mus musculu
Q93356 emericella
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Q9bum4 homo sapien
Q8wuh0 homo sapien
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Q9dby6 mus musculu
Q9bty3 homo sapien
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Q8vhu3 rattus norv
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OL-JUN-2002 (TrEMBLrel. 21, Created)

OL-JUN-2002 (TrEMBLrel. 21, Last sequence update)

OL-JUN-2002 (TrEMBLrel. 21, Last annotation update)

Hypothetical 32.6 kDa protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; ABO
NON TER
SEQUENCE
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Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;
"prediction of the coding sequences of unidentified human genes.XVI.
The complete sequences of 150 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 7.65-73(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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KIAA1324.
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                                                                                                                                                                                                                                                                                                            PTRTENYNESALANTVTLAGGPSFTSKGLKYFHHFTLSLCGNQGRKMSVCTDNVTDLRIP
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                                                                                                                                                                 | IDFWLKVGISAGTCTAILLTVLTCYFWKKNQKLEYKYSKLVMNATLKDCDLPAADSCAIM
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RESULT 3
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                                                                                                           Q42206;
Q42206;
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submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AK055902; BAB71041.1;
InterPro; IPR001891; EGF Ca.
SMART; SM00179; EGF_CA; T.
SMART; SM00179; EGF_CA; T.
SCQUENCE 493 AA; 54595 NW; OAEBB2C19709B211 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Pukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Watsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
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Q96DP2;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 20, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
CDNA FLJ31340 fis, clone MESANI1000035, weakly similar to major surface-labeled trophozoite antigen precursor.
Homo sapiens (Human).
Homo sapiens (Human).
                               01-NOV-1996
01-DEC-2001
Peroxidase (Fragment).
                                                                                    01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                   268 GVAYTSECFPCKPGT 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  882 WREPKLCSGGISLPEGRVTICKTIDFWLKVGISAGTCTAILLTVLTCYFWKKNQKLEYKY 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
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                                                                                                                                                                                                                                                                   43 GVAYTSECFPCKPGT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 SKLVMNATLKDCDLPAADSCAIMEGEDVEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   942 SKLVMNATLKDCDLPAADSCAIMEGEDVEDD 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WREPKLCSGGISLPEORVTICKTIDFWLKVGISAGTCTAILLTVLTCYFWKKNOKLEYKY 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BC022655; AAH22655.1;
                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                (TrEMBLrel. (TrEMBLrel. (TrEMBLrel. )
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                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                               1.5%; Score 15;
100.0%; Pred. No.
                      01,
19,
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              Last sequence update)
Last annotation update)
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                                                                                                                            97 AA.
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hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Length 493;
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    01-JUN-2001
01-JUN-2001
01-JUN-2002
                                          Q9C5R4
Q9C5R4;
                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                 Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                           ProDom; PD186062; HCV_NS1; 1
                                                                                                                                                                                                                                                                       Virology 197:659-668(1993).
InterPro; IPR002531; HCV NS1.
Pfam; PF01560; HCV_NS1; T.
                                                                                                                                                                                                                                                                                                                    Higashi Y., Kakumu S., Yoshioka K., Wakita T., Mizokami M., Ohba K., Ito Y., Ishikawa T., Takayanagi M., Nagai Y.; "Dynamics of genome change in the EZ/NS1 region of hepatitis C virus
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NON_TER
SEQUENCE
                                                                                                                                           132 HGFASLSA 139
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=94069940; PubMed=8249288;
                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome polyprotein [Contains: envelope glycoprotein E2/NS1 (GP68)]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9PXT8;
                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9PXT8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CV. COLUMBIA; TISSUE=SEEDLING; Desprez T., Amselem J., Chiapello H., Caboche M., Hofte Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                  n vivo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00458; PEROXIDASE.
PROSITE; PS00436; PEROXIDASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00141; peroxidase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z29133; CAA82392.1; -. HSSP; P00433; ZATJ.
                                                                                                                      26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          680 VILAGGPS 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 VILAGGPS 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  local Similarity
                                                                                                                    HGFASLSA 33
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 (TrEMBLrel. 17, (TrEMBLrel. 17, 17) (TrEMBLrel. 21,
                                                                                                                                                                                                                  133 AA; 14623 MW; D04D3DC045350488 CRC64;
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                                                      PRELIMINARY;
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100.0%; Pred. No
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Last annotation update)
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             sequence update)
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                                                                                                                                                                                No.
                                                   248 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 AA.
                                                                                                                                                                               DB 12; Length 133;
o. 6.8;
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Matches 8
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Best Local
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Carninci P., Chen H., Cheuk R., Kim C.J., Banh J., Bowser L.,
Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y., Ishida J.,
Carninci P., Chung M.K., Karlin-Neumann G., Kawai J., Lam B., Lee J.M.,
Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M.,
Jin J., Liu S.K., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
Pham P.K., Quach H.L., Sakann H., Sakurai T., Satou M., Seki M.,
Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K., Davis R.W.,
Theologis A., Ecker J.R.;
"Arabidopsis cDNA clones.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8V7G7;
01-MAR-2002
01-MAR-2002
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AT3g49120/T72J13 40.
AT3g49120/T72J13 40.
Arabidopsis thaTiana (Mouse-ear cress).
Arabidopsis thaTiana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; core eudicots; Rosidae;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00141; peroxidase; 1.
PRINTS; PR00458; PEROXIDASE. 2;
PROSITE; PS00436; PEROXIDASE 2;
SEQUENCE 248 AA; 27154 MW; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Analysis of the complete genomes of thirteen TT virus variants classifiable into the fourth and fifth genetic groups, isolated viremic infants.", Arch. Virol. 147:21-41(2002).

EMBL; AB064603; BAB79340.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                               EMBL; AB064603; BAB79340.1; -
InterPro; IPRO04118; TT_ORF2.
Pfam; PF02957; TT_ORF2; 1.
SEQUENCE 302 AA; 32388 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peng Y.H., Nishizawa T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21844401; PubMed=11855633;
Peng Y.H., Nishizawa T., Takahashi M., Ishikawa T., Yoshikawa A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 VTLAGGPS 146
278 DSAAESTG 285
                                                                               145 DSAAESTG 152
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                                                                                                                                                               Conservative 0;
                                                                                                                                                                                                                                                                                                                                    32388 MW;
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L00.0%; Pred. No.
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100.0%; Pred. No. 14
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                        CD492A959881A33C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 AA.
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                                                                                                                                                                                                                                                        DB 12; Length 302;
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                                                                                                                                                                                 Indels
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RESULT 8
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Best Local (
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Q42584; O1-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                    Q9SMU8;
Q9SMU8;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids_II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant Physiol. 104:285-286(1994).
EMBL; X71794; CAA50677.1; -.
HSSP; P00433; ZATJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00435; PEROXIDASE 1; 1.
PROSITE; PS00436; PEROXIDASE 2; 1.
Oxidoreductase; Peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Intapruk C., Takano M., Shinmyo A.;
"Nucleotide sequence of a new cDNA for peroxidase from Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peroxidase (EC 1.11.1.7).
                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last amoutation update)
Peroxidase (Putative peroxidase protein) (AT3949120/T2J13_40).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002016; Peroxidase. Pfam; PF00141; peroxidase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thaliana."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94159792; PubMed=8115548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
 Submitted [4]
             SEQUENCE FROM N.A.

Liu S.X., Sakano H., Pham P.K., Yamada K., Banh J., Etgu
Liu S.X., Sakano H., Pham P.K., Davis R.W., Ecker J.R.,
Toriumi M., Yu G., Shinozaki K., Davis R.W., Ecker J.R.,
"Full Length cDNA of gene T2J13.40 (GI:6522554).";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                              Т2Л13.40.
                                                                                                                                                           Rieger M., Gabel C., Mueller-Auer S., Schaefe
Mewes H.W., Lemcke K., Mayer K.F.X., Quetier I
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 VILAGGPS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    680 VILAGGPS 687
                                                                                                      Submitted
                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                    NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                      Arabidopsis sequencing project; omitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38951 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.8%; Score 8;
100.0%; Pred. N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shinmyo A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8ADC65C72E19B10B CRC64;
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                                                                                                                                                                  , Schaefer M., Zipp M.,
Quetier F., Salanoubat
Bank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                        353 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10;
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                                                   P., Lee J.
Theologis
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                                                                  Lee J.
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Q9A0D7
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Best Local (
 STRAIN=SF370 / ATCC 700294 / SEROTYPE M1; MEDLINE=21192684; PubMed=11296296;
                                                                                                                                     Hypothetical protein SPy0818. SPY0818.
                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                 SEQUENCE FROM N.A.
                                                                               Streptococcaceae;
                                                                                                            Streptococcus pyogenes.
                                                                                                                                                                                                                  Q9A0D7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kim C.J., Chen H., Cheuk R., Meyers M.C., Banh J., Bowser L., Carrinci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
"Arabidopsis ORF clones.", Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
                                                                                                                                                                                                                                     Q9A0D7
                                                               CBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                 139 VTLAGGPS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00435; PEROXIDASE 1; 1. PROSITE; PS00436; PEROXIDASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Myuyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                 680 VILAGGPS 687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin.Neumann G., Kawai J., Kim C., Lam B., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinnzaki K., Davis R.W., Ecker J.R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002016; Peroxidase
                                                                                                                                                                                                                                                                   10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Arabidopsis cDNA clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Theologis A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00141; peroxidase; 1.
S; PR00458; PEROXIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF326880; AAG41462.1; -. AF439700; AAK00382.1; -. AF419569; AAL31901.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AY079106; AAL84990.1; -. P00433; 2ATJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL132967; CAB61998.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length cDNA of gene T2J13.40 (GI:6522554).";
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                                                                                                                                                                                                                                                                                                                                                                                                                                               353 AA;
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                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                       Streptococcus.
PubMed=11296296;
                                                                                                                                                                                                                                                                                                                                                                                                                                               38832 MW;
                                                                                                                                                                                                                                                                                                                                                                           0.8%; Score 8;
100.0%; Pred. No
ntive 0; Misman
                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                           430 AA
                                                                                                                                                                                                                                                                                                                                                                                                         DB 10; Length 353;
                                                                                                                                                                                                                                                                                                                                                                           0,
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AC OCC OCC DTT AC OCC D
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Q9Z891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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MEDLINE=99206606; PubMed=10192388;
Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
"Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
                                                                                                                                                                                                                                                                                                                                                                        Q9Z891;
Q9Z891;
                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                              Chlamydia pneumoniae (Chlamydophila pneumoniae)
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydo
                                                                                                                                                                                                                                                                         Hypothetical protein CPn0458.
                                                                                                                                                                                                                                                                                                                           01-MAY-1999
01-MAY-1999
                                                                                                                                                                               NCBI_TaxID=83558
                                                                                                                                                                                                                                                                                                       01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 PRGDYIAF 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 293:2093-2098(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Samson D., Roux V., Cossart P., Weissenbach J., Raoult D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ogata H., Audic S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21442074; PubMed=11557893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rickettsia conorii.
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TOLB OR RC0406.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rickettsiaceae; Rickettsieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q92IL4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRGDYIAF 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
8; Conserv
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                                                                                                                                                                                                                                                                                      (TrEMBLrel. 10, Created)
(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           430 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Renesto-Audiffren P., Fournier P.-E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48538 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.8%; Score 8;
100.0%; Pred. N
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100.0%; Pred. N
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19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3A0EE0543E53D7F2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5BB9B2223C45B436 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                          695 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ.
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                                                                                                                                                                                         Chlamydophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claverie J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barbe V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>,</u>
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Q9JS58
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AC 04295
DT 01-JU
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GN SPB12
OC Eukar
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EMBL; AE001630; AAD18600.1; -.
Hypothetical protein; Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9JS58 PRELIMINARY; PRT; 695 AA.
Q9JS58; O1-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Hypothetical protein CPJ0458.
CPJ0458 OR CPD294; Oct. Column (CPJ0458)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDITINE-20150255; PubMed=10684935;

Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,

White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,

Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,

Linher K., Weidman J., Khouri H., Craven B., Bowman C., Salzberg S.L.,

Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,

Bisen J., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA.", Nucleic Acids Res. 28:2311-2314(2000).

EMBL; AE002191; AAF38151.1; -.
EMBL; AP002346; BAA98664.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=AR39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=83558;
                                                  01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Hypothetical 82.9 kDa protein C19G7.10C in chromosome
SPBC19G7.10C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   868 VSSCVAGI 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGR; CP0294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20330349; PubMed=10871362;
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                          Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                042958;
                                                                                                                                                                                                                        042958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 8; Conser
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695 AA; 78562 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                 PRELIMINARY;
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100.0%; Pred. No
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446CFFE81014693B CRC64;
                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1F9625881081B670 CRC64;
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                                                                                                                                                                                                                           744 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 16; Length 695; b. 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                 H.
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RESULT 15
Q95XN6
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Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q95XN6 PRELIMINARY; PRT; 77 AA.
Q95XN6 PRELIMINARY; PRT; 77 AA.
Q15XN6 PRECIDENCE PRECIDE PRECIDENCE PRECIDE PRECIDENCE P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein. SEQUENCE 744 AA; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadore
Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical 8.6 kDa protein.
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Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01423; Sm; 1. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                        "Direct Submission.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AC025726; ARX73913.1; -.
InterPro; IPR001163; SNRNP_Sm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence of C. elegans co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "denome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      None;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 642 LKQSGTVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 LKQSGTVN 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                         237 RGNNVLY 243
                                                                                                                                          Local Similarity
les 7; Conserv
65
RCNNVLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MAR-2000)
                                                                                                                                                                                                                                                                                                                  77 AA; 8602 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative .
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82920 MW; 888E06DB42FD92B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           elegans cosmid Y71G12B.";
) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.8%; Score 8;
100.0%; Pred. No
                                                                                                                                                           0.7%; Score 7; DB !
100.0%; Pred. No. 55
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                      805A43965E96C978 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.
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                                                                                                                                                                                                                                             DB 5;
                                                                                                                                                                                                            55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 744;
                                                                                                                                                                                                                                             Length 77;
                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Consortium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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RESULT 16 Q9W2P5 ID Q9W2P5

PRELIMINARY;

PRT;

Q9W2P5;

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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Holt R.A.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Change M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Nelson C.R., Miklos G.L.G.,
RA Man K.H., Doyle C., Baxter E.G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayaktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Betchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dietz S.M.,
RA Godson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley D., Heiman T.J., Hernandez J.R., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wein M.H., Ibegram C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Hostin D., Houston K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Holtin D., Hollshina N.V., Mobarry C., Morris J., Moshreil A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Halazoto M., Pittman G.S., Pan S., Follard J., Puri V., Reese M.G.,
RA Rainert K., Remington K., Sanders R.D.C., Scheeler F., Sakith T.,
RA Mount S.M., Woothers D.A., Weishenbach J.,
RA Halliams S.M., Woothers D.A., Westenbach J.,
RA Palazoto M., Stord R., Sanders R.D.C., Scheeler F., Smith T.,
RA Rainert S.M., Woother J.S., Zhan M., Zhang G., Z
                                                                                                                                                                                                                     Matches
01-JAN-1998 (TrEMBLrel. 05, Created)
                                022823;
                                                022823
                                                                                                                                                                              237 RGNNVLY 243
                                                                                                                                                50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CG9344 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                     Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID≈7227;
                                                                                                                                           RGNNVLY 71
                                                                                                                                                                                                                                                                                            PF01423; Sm;
NCE 79 AA;
                                                                                                                                                                                                                                                                                                                        IPR001163; snRNP_Sm.
                                                                                                                                                                                                              Conservative 0;
                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                 9023 MW; 0480FAC62A4DAF5B CRC64;
                                                                                                                                                                                                          0.7%; Score 7; DB 5
100.0%; Pred. No. 56;
ive 0; Mismatches
                                        91
                                                                                                                                                                                                                                                 DB 5;
                                                                                                                                                                                                                                                 Length 79;
                                                                                                                                                                                                            Indels
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RESULT 18
Q9M1Z3
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                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                     SEQUENCE
                                                                                                EMBL; AL138647; CAB75800.
                                                                                                      EU Arabidopsis sequencing project;
Submitted (FBB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                     D'Angelo M., Vezzi A., Modesto D., Pigazzi M., Valle G., Lemoke K., Mayer K.F.X., Quetier F., Salanoubat M.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core e eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
U6 snENA-associated Sm-like protein.
                                                                             InterPro; IPR001163; snRNP_Sm.
                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                       Q9M1Z3;
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9M1Z3
                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleocapsid; Kibonucica
SROUENCE 91 AA; 9728 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AC002333; AAB64025.1; -. InterPro; IRR001163; snRNP_Sm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01423; Sm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           copennaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Bueil C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Sometville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 RGNNVLY 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lin X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Morganoliophyta; eudicotyledopsis; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Putative small nuclear ribonucleoprotein polypeptide F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 RGNNVLY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
Les 7; Conserv
                                                PF01423; Sm;
NCE 91 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ribonucleoprotein
                                               9913 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0./v;
100.0%; Pr
   100.0%;
                  0.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.7%; Score 7; 1
100.0%; Pred. No.
Score 7; I
Pred. No.
                                             950E3FE402F92045 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22DDFB2C20E23BB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
DB 10;
). 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                 91 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 91;
                                                                                                                                                                                                                                                                                Embryophyta; Tracheophyta;
edons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tracheophyta;
                                                                                                                                                                                                   Mewes H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Matches

7;

Conservative

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Mismatches

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Q9XJP1
                                                                                                                                                           A CONTROL OF THE CONT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                            Query Match
Best Local (
                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-20453452; PubMed=10998166;
De Boever E.H., Clewell D.B., Fraser C.M.;
Enterococcus faecalis conjugative plasmid pAM373; complete nucleotide sequence and genetic analyses of sex pheromone response.";
Mol. Microbiol. 37:1327-1341(2000).
EMBL; AE002565; AAG40455.1;
Hypothetical protein; Plasmid.
SEQUENCE 93 AA; 10366 MW; 344C9A25E2DD1922 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9F1F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Firmicutes; Bacillus/Clostridium group; Lactobacillales;
Enterococcaceae; Enterococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmid pAM373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterococcus faecalis (Streptococcus faecalis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical 10.4 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9F1F2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NUN-2002 (TrEMBLrel. 21, Last annotation update)
proliferating cell nuclear antigen (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1351;
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                                                                                                                                                                                                                                                                                                                "Proliferating cell nuclear antigen in the brown tide alga."; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF126735; AAD29399.1; -.
HSSP; P12004; 1AXC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9XJP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9XJP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; stramenopiles;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=PT-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aureococcus anophagefferens
                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                   NON
                                                                                                                                                                                                                                 InterPro; IPR000730; Pr cel_nuc_antig. Pfam; PF0747; PCNA_C; 1. Probom; PD002673; Pr_cel_nuc_antig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                       NON_TER
  788 ESLGIPD 794
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7; Conserva
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100 AA;
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                                                     Conservative
                                                                                                                                                              11104 MW; 0579A7DA2EF0C773 CRC64;
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100.0%; Pred. No.
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100.0%; Pred. No.
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                                                                                                              DB 10; Length 100;
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MEDITURE-2157209, PubMed=11463916;

Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,

Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,

Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,

Umayam I.A., White O., Salzberg S.L., Lewis M.R., Radune D.,

Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,

McDonald I.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey F.

McDonald I.A., Feldblyum T.V., Angiuoli S., Venter J.C.,

Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,

Bougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;

"Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein SP0650.
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Q1-QCT-2001 (TrEMBLrel. 18, Created)
Q1-QCT-2001 (TrEMBLrel. 18, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae.
Bacteria, Firmicutes, Bacillus/Clostridium group, Lactobacillales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 293:498-506(2001).
EMBL; AE007374; AAK74796.1; -.
TIGR; SP0650; -.
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NON_TER
SEQUENCE
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Possible kiaa0568 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Complete proteome.
SEQUENCE 106 AA; 12657 MW; 4C32886B5AAB7572 CRC64;
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                                                                                                                                                                                        Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AL390935; CAC00863.1; -.
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                                                                                                                                                                                                                                                                                                                                                         sukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
1951_TaxID=5664;
                                                                                                                                                                                                                                                                              STRAIN=FRIEDLIN;
                                                                                                                                                                                                                                                                                                               EQUENCE FROM N.A.
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115 AA;
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L00.0%; Pred. No.
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o. 73;
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                                                           DB 5;
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Q9M280
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                                                                                  MEDLINE-20055654; PubMed=10589737; Marchenko G.N., Marchenko N.D., Tsygankov Y.D., Chistos "Organization of threonine biosynthesis genes from the methylotroph Methylobacillus flagellatus."; Microbiology 145:3273-3282(1999).

EMBL; L78665; AAF21127.1; -.
EMBL; L78665; AAF21127.1; -.
SEQUENCE 122 AA; 13500 MW; 7D8E0F4621303693 CRC64;
                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EU Arabidopsis sequencing project; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; tAl138641; CAB86923.1; -.
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Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes
Rieger K., Mayer K.F.X., Quetier F., Salanoubat M.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 Membrane protein.
                                                                                                                                                                                                      NCBI_TaxID=405;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein. SEQUENCE 116 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
             827 PGSLLLP 833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3702;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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                                                         Local Similarity
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PGSLLLP 43
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100.0%; Pred. No. 79;
tive 0; Mismatches
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100.0%; Pred. No
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Last sequence update)
Last annotation update)
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Mismatches
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                                                    DB 2;
o. 82;
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Q97UE3 Q97UE3;

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RESULT 27
Q97UE3
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Q94045;
01-FEB-1997
01-FEB-1997
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                   Chen Q., Wahlgren M.;
Submitted (DEC-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                               EMBL; AF039280; AAD02163.1;
                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum.
Eukaryota; Alveolata;
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Erythrocyte membrane protein FCR3S1.2VAR8.
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                                                                                                                       529 KGSKGKQ 535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003173; PC4. Pfam; PF022229; PC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z81122; CAB03353.1;
HSSP; P53999; 1PCF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
NCBI TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T13F2.2.
Caenorhabditis elegans.
Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 609 YYIDRDS 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Genome sequence of the nematode C.elegans: A platform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 me;
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                                                                                 85
                                                                                                                                                                 Local Similarity
tes 7; Conserv
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nes 7; Conserv
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                                                                                                                                                                                                                                                   132
132 AA;
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(TrEMBLrel. 02,
(TrEMBLrel. 19,
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100.0%; Pred. No. 83;
ive 0; Mismatches
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Caenorhabditis.
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ESTRAINATCC 35092 / DSM 1617 / P2; /*

CSTRAINATCC 35092 / DSM 1617/P2;

X MEDLINE=2132296; PubMed=11427726;

X AMPLINE=2132296; PubMed=11427726;

X She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

X AMAYEZ M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

X AMAYEZ M.J., Chan-Weiher C.C., Coordon P.M.K.,

X De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

X Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

X Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

X Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

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X Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

X Heikamp-d
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Best Local :
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Hypothetical protein; Complete SEQUENCE 134 AA; 15459 MW;
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01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21153631; PubMed=11254626;
Haneda T., Okada N., Nakazawa N., Kawakami T., Danbara H.;
"Complete DNA Sequence and Comparative Analysis of the 50-Kilobase
"Complete Plasmid of Salmonella enterica Serovar Choleraesuis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella enterica subsp. enterica serovar Choleraesuis.
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                                                                                                                                                                                                                                                                                                                                               Infect. Immun. 69:2612-2620(2001).
EMBL; AB040415; BAB20547.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=RF-1
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                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                         Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                      491 NKEVARI 497
93
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   NKEVARI
                                                                                                                                 l Similarity
7; Conserva
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(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                    138 AA;
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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                                                                                                                                 100.0%; F1
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                                                                                                                                                                                                                                                                                    16387 MW;
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100.0%; Pred. No.
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E0CAC16D74E039A5 CRC64;
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o. 89;
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                                                                                                                                                                                                              Length 138;
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RESULT 29 005567

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Matches 7; Conserv
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01-NOV-1998 (TEMBLrel. 08, La
Hypothetical 15.8 kDa protein.
MLCB33.17.
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005567;
01-JUL-1997
01-JUL-1997
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Submitted (APR-1997)
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EMBL; Z94723; CAB08133.1; -.
Hypothetical protein.
SEQUENCE 141 AA; 15792 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                         Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M., Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J., Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-Isenbarger T.A., Jeck R.F., Pohlschroder M., Spudich J.L., Jung K.-Baham M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebhardt H., Lowe T.M., Lidang P., Riley M., Hood L., DasSarma S.; "Genome sequence of Halobacterium species NRC-1."; "Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteria;
Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9HRJ4;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9HRJ4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93188700; PubMed=8446027;
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                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. EMBL; AE005013; AAG19164.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=64091;
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                                                                                                 159 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
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       Conservative
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100.0%; F1
                                                                                                   15971 MW;
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100.0%; Pred. No.
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b; Pred. No. 93;
0; Mismatches
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                                                                                                      BCC586A96222C254 CRC64;
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                                                        DB 17;
                                  1e+02;
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28 LLLWAGT 34

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RESULT 32
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      Query Match
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                                                                                                                                                                                                                    Cryptosporidium muris.
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
                                             NON_TER
                                                                    "Sequence Differences in the Diagnostic Target Region of the Oocyst Wall Protein Gene of Cryptosporidium Parasites.", Appl. Environ. Microbiol. 66:5499-5502(2000).

EMBL, AF266264; AAG39045.1; -
InterPro; IPR002086; Aldehyde dehydr.
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Q9U732
Q9U732;
Q1-32
Q9U732;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-CCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Q0Cyst wall protein (Fragment).
Cryptosporidium serpentis.
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
                                                                                                                                                                                                                                                                                                                        Q9GQD9;
01-MAR-2001
                                 SEQUENCE
                                                                                                                                                          Xiao L
                                                                                                                                                              MEDLINE=20551138; PubMed=11097936;
                                                                                                                                                                                  STRAIN=34
                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                  NCBI_TaxID=5808;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRÓUENCE FROM N.A.

MEDLINE-99437830; PubMed=10508071;

Sulaiman I.M., Xiao L., Lal A.A.;

"Evaluation of cryptosporidium parvum genotyping techniques.";

Appl. Environ. Microbiol. 65:4431-4435(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                            CPPNTIL 99
                                                                                                                                              ., Limor J., Morgan U.M., Sulaiman I.M., Thompson R.C.A.,
                                                         PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
                              163
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163 AA;
                                                                                                                                                                                                                                                                                     (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                             163
                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                              AA;
                            17295 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.7%; Score 7; I
100.0%; Pred. No.
tive 0; Mismatc
  0.7%; Score 7;
                        734E427DCFB9D19E CRC64;
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                                                                                                                                                                                                                                                                                                                                            163 AA.
 DB 5;
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Length 163;
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ID Q83X6

AC Q83X6;

AC Q83X6;

DT 01-UUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-UUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-UUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Disease resistance-like protein 17-36 (Fragment).

OS Mentha longifolia (Horse mint).

OE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Lamiales; Lamiaceae; Mentha.
     Q9U733
ID Q
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                              RESULT 35
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Q8S448
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SEQUENCE
     Q9U733
                                                                                                                                                                                                        EMBL; AF474173; AAL83251.1; -.
                                                                                                                                                                                                                   Davis T.M., Vining K.J., Smith C.A., Zhang Q., Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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NON_TER
NON_TER
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                                                                                          787 LESLGIP 793
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Disease resistance-like protein 585-6 (Fragment).
Mentha longifolia (Horse mint).
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Q8S448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Lamiaceae; Mentha
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                                                                 87 LESLGIP 93
                                                                                                                   Local Similarity nes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                    165 AA;
                                                                                                                                                                                   165
                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 AA;
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 PRELIMINARY;
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                                                                                                                                                                18312 MW; 91BB59DD313239C2 CRC64;
                                                                                                                              0.7%; Score 7;
100.0%; Pred. No.
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100.0%; Pred. No
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); Mismatches 0;
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167 AA.
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o. 1.1e+02;
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RESULT 36
Q9GQE
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AC Q9GQE
DT 01-MA
DT 01-JU
DD 00CY9
GN 0WP.
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CCrypt
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
0ccyst wall protein (Fragment).
Cryptosporidium muris.
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
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01-MAR-2001
01-MAR-2001
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EMBL; AF161579; AAF04005.1; -...
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InterPro; IPR002086; Aldehyde dehydr.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
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Q9GQC8;
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Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
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Xiao L., Limor J., Morgan U.M., Sulaiman I.M., Thompson R.C.A.,
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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01-MAY-2000
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Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
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STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
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131 ÖSYTYİİ 137
                                                                                    535 QSYTYII 541
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1.1e+02;
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                      Query Match
Best Local :
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                                                                     NON TER
                                                          SEQUENCE
                                                                                    Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF134401; AAD24480.1; -.
                                                                                                                    SEQUENCE FROM N.A.
TISSUB=TESTIS;
Bartles J.R., Zheng L., Li A., Wang M.;
"Organization and chromosomal location of the espin gene in the
                                                                                                                                                                                                                        Putative espin (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last seq
01-NOV-1999 (TrEMBLrel. 12, Last ann
                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON TER
                                                                                                                                                                                                                                                                                          Q9Y329;
                                                                                                                                                                                                                                                                                                       Q9Y329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Large-scale screening of intracellular protein localization in living fission yeast cells by the use of a GFP-fusion genomic DNA library."; Genes Cells 5:169-190(2000).

EMBL; AB027973; BAA87277.1; -.
HSSP; P21707; 1BNN.
                                                                                                                                                                                      CBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00499; C2_DOMAIN_1; UNKNOWN_1.
PROSITE; PS50004; C2_DOMAIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 21.0 kDa protein (Fragment)
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                       954 DLPAADS 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ptam; PF00168; C2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ding D.Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20223868; PubMed=10759889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
       Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                121 DLPAADS 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; PR00360; C2I
SM00239; C2;
                                                      192 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 AA;
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       Conservative
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                                                 21971 MW; 44236A20760AEEF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        21013 MW; 59E63D8C2BED8750 CRC64;
  0.7%; Score 7; 1
100.0%; Pred. No.
tive 0; Mismatcl
                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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100.0%; Pred. No. 1.2e-
                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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     Mismatches
              DB 4; Len
o. 1.2e+02;
                                                                                                                                                                                                                                                                                                192 AA.
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                        Length 192;
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EMBL; U83136; AAB61906.1; -...
InterPro; IPR003439; ABC transportr.
Pfam; PF00005; ABC tran; 1.
ProDom; PD000006; ABC transportr; 1.
TIGRPAMs; TIGR01189; CcmA; 1.
                                                                    Patterson C.S., Donohue T.J., "Identification and characterization of putative cytochrome c maturation genes (ccmABCDG) from Rhodobacter sphaeroides.", Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=2.4.1;
                                                                                                                                                                                                            Bacteria; Proteobacteria; alpha
                                                                                                                                                                                                                      Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides)
                                                                                                                                                                                   NCBI_TaxID=1063;
                                                                                                                                                                                                                                                          Hypothetical ABC transporter
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Pfam; PF01551; Peptidase M37; T.
Hypothetical protein; Complete proteome.
SEQUENCE 197 AA; 21348 MW; 7E0A29BC0874CC50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9RWR8;
Q9RWR8;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20036896; PubMed=10567266; White O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., White O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Bemphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Vantarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE001918; AAF10178.1; -. TIGR; DR0598; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.", Science 286:1571-1577(1999).
                                                                                                                                                                                                                                                                                                                                                                                                              179 İYTAAGA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                            458 IYTAAGA 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein DR0598.
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01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deinococcus radiodurans.
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100.0%; Pred. No. 1.3e+02;
ive 0; Mismatches 0;
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                                                                                                                                                                                                      subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                 210 AA.
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Best Local
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DIC-2002 (TrEMBLrel. 21, Last annotation update)
Putative integral membrane protein.
SCO1316 OR SCBAC36F5.27C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE=97000351; PubMed=8843436; Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.; Kinashi H., Hopwood D.A.; Bet of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
STRAIN=A3(2);
STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                STRAIN=A3(2) / M145;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                    coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL592292; CA642863.1; -.
InterPro; IPR000252; DedA.
InterPro; IPR000794; Ketoacyl-synt.
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                 "Complete genome sequence of the model actinomycete Streptomyces
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                                                                                                                                                         Pfam; PF00597; DedA; 1
                               787 LESLGIP 793
25
                                                                         Local Similarity
   LESLGIP 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS00211; ABC_TRANSPORTER; UNKNOWN_1.
210 AA; 21817 MW; 72C42BE3B1804D
                                                                                                                           PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
211 AA; 22286 MW; 1A0F8EA70072A6A4 CRC64;
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                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parkhill J., Barrell'B.G., Rajandream M.A.
N-2001) to the EMBL/GenBank/DDBJ databases.
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100.0%; Pred. No.
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                                                                  Mismatches
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                                                                                DB 16; L
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                                                                  0; Indels
                                                                                                 Length 211;
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RESULT 44
Q8ZIP0
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01-MAR-2002 (TrEMBLrel. 20, Last
01-JUN-2002 (TrEMBLrel. 21, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Basker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quall M., Rutherford K., Skelton J., Stevens K., Whitehead S., Barrell B.G., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., G., Charles M., Rutherford K., Charles M., Skelton J., Stevens K., Whitehead S., Barrell B.G., G., Charles M., Rutherford M., Rutherford M., Skelton P.C.F., Quall M., Rutherford M., Charles M., Skelton P.C.F., Quall M., Rutherford M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles M., Charles
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yersinia pestis.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Brandon R.C., Baldwin D., Andrews-Pfannkoch C., Baldwin D., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001345; PG/BPGM_mu
Pfam; PF00300; PGAN; 1
PROSITE; PS000175; PG_MUTASE; 1.
Isomerase; Hypothetical protein
SEQUENCE 215 AA; 23829 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of Yersinia pestis, the causative agent of plague.", Nature 413:523-527\,(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21470413; PubMed=11586360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9VV45;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ414142; CAC89311.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CG12255 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9VV45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phydroidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BIOVAR ORIENTALIS;
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23829 MW; B59BC554434E47FB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 7; DB 1
%; Pred. No. 1.4
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.4e+02;
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RESULT 46
Q94LR6
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., VanAken S.E., Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L., White O., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 23.5 kDa protein.
Oryza sativa (Rice).
                                                                                                                                         "Oryza sativa chromosome 10 BAC OSJNBb0011A08 genomic sequence.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC034258; AAK54290.1;
                                                                                                            SEQUENCE
                                                                                                                               Hypothetical
                                                                                                                                                                                                                                                                                                                             STRAIN=CV. NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4530;
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InterPro; IPR000618; Insect cuticle.
Pfam; PF00379; Chitin_bind_4; 1.
SEQUENCE 217 AA; 24162 MW; D3624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          343 DANGETO 349
                                    Local Similarity
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                                                                                                al protein.
223 AA; 2
                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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    0./08; Pi
                                                                                                  23534 MW;
    0.7%; Score 7; DB 1
100.0%; Pred. No. 1.4
ive 0; Mismatches
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100.0%; Pred. No.
tive 0; Mismatcl
                                                                                             02C547E08745A473 CRC64;
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                          DB 10; Le
o. 1.4e+02;
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                                                Length 223;
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Gaps
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RESULT 48
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Q9ZK02
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                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                  Write O., Dodson R., Hickey E.K., Gwinn M., Peterson J., van-Vugt F
Palmer N., Haft D., Rosa F., Stevenson B.,
"A bacterial genome in flux: The twelve linear and nine circular
extrachromosomal DNAs in an infectious isolate of the Lyme disease
                                                                                                                                                                                                                                                        Q9S0D9
Q9S0D9;
spirochete Borrelia burgdorferi.";
Mol. Microbiol. 0:0-0(1999).
                                                                                                                           Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
NCBI_TaxID=139;
                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel 13,
01-MAY-2000 (TrEMBLrel 13,
01-JUN-2001 (TrEMBLrel 17,
                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                      Plasmid
                                                                                                                                                              Borrelia burgdorferi (Lyme disease spirochete).
                                                                                                                                                                                               Outer surface protein F.
                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00228; TUBULIN B AUTOREG; 1.
GTP-binding; Microtubules; Complete proteome.
SEQUENCE 223 AA; 25325 MW; E857C9DD8F676D9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 397:176-180(1999).

-I- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES.

BINDS TWO MOLES OF GTP, ONE AT AN EXCHANGEABLE SITE ON THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99120557; PubMed-9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis
                                                                                                                                                                                                                                                                                                                                                                        973 LIFTSKN 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE001542; AAD06731.1; -.
InterPro; IPR002453; Beta tubulin.
InterPro; IPR003754; HEM4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria, Proteobacteria, epsilon subdivision, Helicobacter group,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative uroporphyrinogen-III synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genomic sequence comparison of two unrelated isolates of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HEMD OR JHP1145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9ZK02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9ZK02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1999
                                                                                                                                                                                                                                                                                                                                             38 LIFTSKN 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       460 TAAGASD 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 TAAGASD 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BINDS TWO MOLES OF GTP, ONE AT AN EXCHANCHAIN AND ONE AT A NONEXCHANGEABLE SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TaxID=85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF02602; HEM4;
                                                                                                                                                      cp32-4.
                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                          100.0%; F1
                                                                                                                                                                                                                                                                                                                                                                                                          0.7%; Score 7; DB 16; London 1.4e+02;
                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                                                   224 AA.
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                                                                              REGULATORS.

REGULATORS.

REMBL; AL591083; CAC37887.1; -.

InterPro; IPR001647; HTH TetR.

Pfam; PF00440; tetR; 1.

DNA-binding; Transcription regulation.

DNA-binding; AA; 24083 MW; B341DBD4/
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InterPro; IPR003483; OspEF.
Pfam; PF02471; OspEF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=A3(2) / M145;
Bentley S.D., Chatcr K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q93S03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Firmicutes, Actinobacteria, Actinobacteridae,
Actinomycetales, Streptomycineae, Streptomycetaceae, St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q93S03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97000351; PubMed=8843436; Redenbach M., Kieser H.M., Denapaite D., Eichner A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Actinomycetales; Streptomycineae; NCBI_TaxID=1902;
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                                                                                                                                                                                                                                                                       "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
-!- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         Hopwood
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7; Conserv
Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harris D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parkhill J.,
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                             0.7%; Score 7;
100.0%; Pred. No.
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Pred. No. 1.4e+02;
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                                                                                                                  B341DBD44A209CB4 CRC64;
        Mismatches
                                                          DB 16; Length 224;
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                                   1.4e+02;
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042826;
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Bukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1998 (TrEMBLrel. 06,
01-JUN-1998 (TrEMBLrel. 06,
01-OCT-2001 (TrEMBLrel. 18,
                                                                                                   025822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pdh1 protein precursor.
PDH1 OR SPCC1235.08C.
                                                                                                                                                                                                                                                             DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE=98162726; PubMed=9501995;
Tha H., Takimoto M., Danjoh I., Pujiyama A.;
"Identification and characterization of a novel trans-membrane protein
gene, pdh1, from Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4896;
                                                         01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
Uroporphyrinogen III COSYNTHASE (HEMD).
                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                        ÉMBL; AL031764;
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
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                                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Res. 4:393-396(1997).
                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
NCBI_TaxID=210; [1]
                                                                                                                                                                                                                                                                                                                 TRANSMEM
                  Helicobacter
                            Bacteria; Proteobacteria; epsilon subdivision;
                                        Helicobacter pylori (Campylobacter pylori);
                                                                                                                                                                                                                                                                                                                                                                                                          ood V., Rajandream M.A., Baubmitted (SEP-1998) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24
                                                                                                                                                                  214 ELFHLES
                                                                                                                                                                                      783 ELFHLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLWRLLL
                                                                                                                                                                                                                                                                                                                                                                                                 D88384; BAA24946.1;
                                                                                                                                                                                                           l Similarity
7; Conserv
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                                                                                                                                                                                                            Conservative
                                                                                                                PRELIMINARY;
                                                                                                                                                                                        789
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27
27
42
63
87
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41
62
65
86
97
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100.0%; Pre
                                                                                                                                                                                                                                                      26021 MW;
                                                                                                                                                                                                                                                                                                                                                                                                              INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                         Barrell B.G., Murphy L., Harr
ne EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                      Score 7;
                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
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                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
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                                                                                                                   226 AA
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                                   Helicobacter group;
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RESULT 52
Q9MP30
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Best Local
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                                                                                                                                                                          Chiotis M., Jermiin L.S., Crozier R.H.;
"A molecular framework for the phylogeny of the ant subfamily Dolichoderinae.";
                                                                                                                                                                                                                   STRAIN=ACLP;
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                   Pterygota; Neoptera; Endopte
Formicidae; Dolichoderinae;
                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                             Mitochondrion.
                                                                                                                                                                                                                                                                                                                                              Cytochrome b (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                             Q9MP30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPRO02453; Beta tubulin.
InterPro; IPRO03754; HEM4.
Pfam; PF02602; HEM4; 1.
PROSITE; PS00228; TUBULIN B AUTOREG; 1.
PROSITE; PS00228; TUBULIN B AUTOREG; 1.
GTP-binding; Hypothetical protein; Microtubules; Complete proteome.
SEQUENCE 226 AA; 25862 MW; 82BAF4B54D6AFEBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
-!- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
EMBL; AE000628; AAD08269.1; -.
TIGR; HP1224; -.
                                                                                                                                                                                                                                                                                                                        Forelius chalybaeus.
                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                   Q9MP30;
                                                                                                                                                                                                                                                       NCBI_TaxID=121505;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=26695 / ATCC 700392;
MEDLINE=97394467; PubMed=92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter J.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES. BINDS TWO MOLES OF GTP, ONE AT AN EXCHANGEABLE SITE ON THE CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIFTSKN
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                                                                                                                                                                                                                                                                               Endopterygota; Hymenoptera; Apocrita; Aculeata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.7%; Score 7; DB 1
100.0%; Pred. No. 1.4
tive 0; Mismatches
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Last
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annotation update)
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o. 1.4e+02;
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RESULT 54
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Q8SUT3
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01-JUL-1997
01-DEC-2001
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Q8SUT3;
Q1-JUN-2002 (TrEMBLrel. 21, Created)
Q1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                   007821;
                                                                                                                                                                                                                                                                                                                            007821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence and gene compaction Encephalitozoon cuniculi.", Nature 414:450-453 (2001).
EMBL, AL590448, CAD26335.1; -.
MEDLINE=95014061; PubMed=7928987;
                          SEQUENCE FROM N.A.
STRAIN=GB17;
                                                                                                                                    Bacteria; Proteobacteria;
                                                                                                                                                               Paracoccus denitrificans
                                                                                                                                                                                                     Flavoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein SEQUENCE 246 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21576510; PubMed=11719806;
Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P.,
Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
Weissenbach J., Vivares C.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genoscope;
Submitted (APR-2001)
                                                                                      NCBI_TaxID=266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-GB-M1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
NCBI_TaxID=6035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Encephalitozoon cuniculi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    469 FMILTLV 475
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                                                                                                                                                                                                                             (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                        (Fragment)
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100.0%; Pre
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04,
                                                                                                                               alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
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Pred. No.
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Pred. No
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5. 1.5e+02;
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HSSP; Q06530; 1FCD.
NON TER 247 247
SEQUENCE 247 AA; 26445
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NCBI_TaxID=5664;
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ
EMBL; AL359774; CAB95228.2; -.
EMBL; AL359683; CAC37117.1; -.
"Genome sequence of the hyperthermophilic crenarchaeon aerophilum.", Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002). EMBL; AE009818; AAL63440.1; InterPro; IPR003794; DUP191.
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Bukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
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"Cloning and expression of Penicillium
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Lin L., Xie B.-F.,
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                                                                                                                                                           STRAIN=IM2
                                                                                                                                                             SEQUENCE FROM:N.A.
STRAIN=IM2 / ATCC 51768 / DSM 7523;
                                                                                                                                                                                                                                       Archaea; Crenarchaeota; Thermo
Thermoproteaceae; Pyrobaculum
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                                                                                                                                          PubMed=11792869;
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b. 1.6e+02;
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RESULT 59
Q92TZ9
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                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative modification methylase protein.
HEMK2 OR RB1344 OR SMB21514.
Phizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymB (megaplasmid 2).
Bacteria; Proteobacteria; alpha subdivision; Rhizob
                                                                                                                                                    Q92TZ9;
                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence and gene compaction Encephalitozon cuniculi.", Nature 414,450-453 (2001).
EMBL; AL590450; CAD25919.1; -. EMBL; AL590445; CAD26684.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21576510; PubMed=11719806;
Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M., Weissenbach J., Vivares C.P.;
                        Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein. SEQUENCE 268 AA; 3
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Submitted (APR-2001) to the EMBL/Genfank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein ECUI1_0090 (Hypothetical protein ECU05_1640).
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PROSITE; PS00136; SUBTILASE ASP; UNKNOWN 1.

Hypothetical protein; Complete proteome.

SEQUENCE 267 AA; 29602 MW; 08362C2A1FE0C293 CRC64;
NCBI_TaxID=382;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=GB-M1;
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NCBI_TaxID=6035;
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Pfam; PF02642; DUF191; 1.
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100.0%; Pred. No.
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100.0%; Pred. No. 1.0
tive 0; Mismatches
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o. 1.6e+02;
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                                 Rhizobiaceae group;
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RESULT 61
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Q&YSU3
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Q8U7C6 PRELIMINARY; PKT; 20% Am.
Q8U7C6;
Q1-JUN-2002 (TrEMBirel. 21, Created)
O1-JUN-2002 (TrEMBirel. 21, Last sequence update)
O1-JUN-2002 (TrEMBirel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21595285; PubMed=11759840;
KAIDENCE FROM N.A.
KAIDENCE T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.;
"Complete genomic sequence of the filamentous nitrogen-fixing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8YSU3;
Q8YSU3;
01-MAR-2002
01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical SEQUENCE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cyanobacterium Anabaena sp. strain DNA Res. 8:205-213(2001).
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Bacteria; Cyanobacteria; Nostocales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AP003591; BAB74688.1; -.
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ALL2989.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete sequence of the 1,683-kb pSymB megaplasmid fixing endosymbiont Sinorhizobium meliloti.";
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                                                                                                                                                                                                                                       204 KAGVSSQ 210
                                                                                                                                                                                                                                                                                   752 KAGVSSQ 758
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                                                                                                                                                                                                                                                                                                                                                                                                                          cl protein; Complete proteome.
282 AA; 31531 MW; 7EBC9ADCD7A119AE CRC64;
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0; Mismatches
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b. 1.7e+02;
ches 0;
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Kimura T.,
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RESULT 62
Q9P451
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Best Loc
Matches
                                                                                                            SEQUENCE FROM N.A.

SPECIES=P.Cyclopium; STRAIN=PG37;
Wu M., Qian Z., Min T., Sun C., Huang W.;
"Cloning and sequencing of alkaline lipase cDNA from Penicillium cyclopium PG37.";
cyclopium PG37.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21608550, PubMed=11743193;

Mood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Chapman P., Clendenning J., McClelland E., Palmieri A.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Romero P., Gordon D.

Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.

Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,

Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 17, Last sequence update)
01-OCT-2000 (TrEMBLrel. 17, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last sequence update)
Alkaline lipase (EC 3.1.1.3) (Triacylglycerol lipase precursor).
Penicillium cyclopium, and
Penicillium expansum.
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
NCBI_TaxID=60167, 27334;
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Q9P451;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58."; Science 294:2322-2328 (2001). Science 294:2328-2328 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goodner B., Hinkie G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L. Houmiel K., Gordon J., Vaudin M., Iartchouk O., Egp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nester E.W.; "The genome
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Agrobacterium tumefaciens
Bacteria; Proteobacteria;
Rhizobiaceae; Rhizobium.
                           Wu M., Qi
"Cloning
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                                                SPECIES=P.expansum; STRAIN=WMC20718; Wu M., Qian Z., Min T., Sun C., Huans
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and sequencing
WMC20718.";
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                     Sun C., Huang W.; of alkaline lipase
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o. 1.7e+02;
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Rhizobiaceae group;
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Best Local S
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Graves T., Wohldmann P
"The sequence of C. el
Submitted (OCT-1996) t
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Q94295;
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EMBL; AF288685; AAF99329.1; --
EMBL; AF398655; AXK07480.1; --
InterPro; IPR002921; Lipase_3.
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                                                                                                                         Submitted (JUL-2001) to the EMBL/GenBank/DDBJ EMBL; U70858; AAB09178.1; -. InterPro; IPR000276; GPCR Rhodpsn. PROSITE; PS50262; G PROTEIN_RECEP_F1_2; 1.
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                                                                                     Hypothetical SEQUENCE 2
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                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the nematode C. investigating biology. The C. elegascience 282:2012-2018(1998).
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                                                                                                                                                                                                                 Direct Submission.";
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                                                                                        al protein.
294 AA; 3
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(TrEMBLrel. 02, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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      0.7%; S llarity 100.0%; Conservative 0;
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Shi Q.Q., Lin C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kDa protein.
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to the
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                          Score 7; I
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EMBL/GenBank/DDBJ databases.
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TRIACYLGLYCEROL LIPASE.
; C2D27E91C7557D14 CRC64;
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           Mismatches
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Q9AB93
ID Q9AB9
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 Wu K., Chung L., Revill W.P., Katz L., Reeves C.D., "The FK520 gene cluster of streptomyces hygroscopicus var. ascomyceticus (ATCC 14891) contains genes for biosynthesis of unusual
                                                                                                        Streptomyces hygroscopicus var. ascomyceticus.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                    MEDLINE=20323220; PubMed=10863099;
                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                         Q9KIFO;
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-i - SIMILARITY: TO OTHER ALPHA SUBUNITS OF SUCCINYL-COA SYNTHETASE, OF EMEL; AEBOS-TO; AAKZ3325.1; -.
                                                                                                                                                                                                            01-OCT-2000
                                                                                                     NCBI_TaxID=132248;
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PROSITE; PS01216; SUCCINYL COA LIG 1; 1.
ATP-binding; Ligase; Phosphorylation; Tricarboxylic acid cycle;
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InterPro; IPR000303; CoA ligase.
Pfam; PF002629; CoA binding; 1.
Pfam; PF00549; ligase-CoA; 1.
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STRAIN=ATCC 19089 / CB15;
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01-JUN-2002
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extender units.";
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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100.0%; Pred. No. 1.5
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Best Local
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InterPro; IPR003781; CoA binding.
InterPro; IPR003781; CoA Ligase.
Pfam; PF02629; CoA binding; 1.
Pfam; PF02629; CoA binding; 1.
Pfam; PF0549; ligase-CoA; 1.
TICREAMS; TICRO1019; SUCCOMALDHA; 1.
PROSITE; PS01216; SUCCINYL COA LIG 1; 1.
PROSITE; PS00399; SUCCINYL COA LIG 2; 1.
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Best Local
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     01-MAR-2002
01-MAR-2002
01-JUN-2002
                                           Q8ZLB0;
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-!- SIMILARITY: TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.
EMBL, AF23504; AAF86383.1; -.
InterPro; IPRO00847; HTH LysR.
InterPro; IPR005119; LysR subst.
Pfam; PF00126; HTH 1; 1.
Pfam; PF00126; HTH 1; 1.
Pfam; PF001366; LysR substrate; 1.
PRINTS; PR00039; HTHLYSR.
PROSITE; PS00044; HTH LYSR FAMILY; UNKNOWN_1.
DNA-Binding; Transcription regulation.
SEQUENCE 297 AA; 32462 MW; D015FBD4AC59A19D CRC64;
                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                     Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
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Phyllobacteriaceae; Mesorhizobium.
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01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                     Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
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                                                                                                                      187 DPVKGTE 193
                                                                                                                                                                                                                                                                                                                                                                          "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21082930; PubMed=11214968;
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STRAIN-LT2 / SGSC1412 / ATCC 700720;

MEDLINE-21534948; PubMed-11677609;

MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,

Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,

Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,

Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,

Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CO-92 / BIOVAR ORIENTALIS;
MEDDINE=21470413; PubMed=11586360;
MEDDINE=21470413; PubMed=11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Peltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome sequence of Yersinia pestis, the causative agent of plague."
Nature 413:523-527(2001).
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8ZA21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=632;
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Pfam; PF00528; BPD_transp; 1.
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Complete proteome.
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100.0%; Pred. No.
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b. 1.8e+02;
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RESULT 70
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
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O1-MAR-2002 (TrEMBLrel. 20, Created)
O1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                              OBUC61 PRELIMINARY; PRT; 300 AA.

OBUC61;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Succinyl-COA synthetase alpha chain.
SUCD OR ATUZ637 OR AGR C 4779.
SUCD OR ATUZ637 OR AGR C 4779.
Agrobacterium tumefaciens (strain C58 / ATCC 33970)
Agrobacterium tumefaciens (strain C58 / ATCC 33970)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
EMBL; AL627281; CBD07995.1; -.
InterPro; IPR000515; BPD_transp.
Pfam; PF00528; BPD_transp; 1.
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                                                                        MEDLINE-2160550; PubMed=11743193;
MEDLINE-2160550; PubMed=11743193;
Mood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Okura V.K., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyarin T., Levy R., Li M.-J., WcClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Chunley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
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                                                                                                                                                                                                                                                                                                                     Rhizobiaceae; Rhizobium.
NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; alpha subdivision;
Science 294:2317-2323 (2001).
                                    "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                         Nester E.W.;
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A Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
A Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
A Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
A Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.,
A Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.,
A Proc. Mat. Proc. A Control Sci. U.S.A. 98:9877-9882(2001).
B EMBL, AL591792; CCA47633.1; ---
DR Interpro, IPR003781; CCA binding.
Interpro, IPR003781; CCA binding.
Interpro, IPR00303; COA ligase.
DR Pfam; PP02629; COA binding; 1.
DR Ffam; PP02629; COA binding; 1.
DR Ffam; PP02629; COA binding; 1.
DR Ffam; PP02639; SUCCINYL COA LIG 1; UNKNOWN 1.
DR PROSITE; PS00399; SUCCINYL COA LIG 2; UNKNOWN 1.
DR PROSITE; PS00399; SUCCINYL COA LIG 2; UNKNOWN 1.
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Best Local
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
187 DPVKGTE 193
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01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21608551; PubMed=11743194;
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SEQUENCE FROM N.A.
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E 300 AA; 30927 MW;
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RESULT 72

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RESULT 73
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Best Local :
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Q9Z799;
Nucleic Acids Res. 28:2311-2314(2000).
             Shiral M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T., "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA.";
                                                                                                                                         MEDIJINE=9206606; PubMed=10192388;
MEDIJINE=9206606; PubMed=10192388;
Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
Kalman S., Grimwood J., Davis R.W., Stephens R.S.;
"Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
                                                                                                                                                                                                                                                                                                                         01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last seq
01-UNN-2001 (TrEMBLrel. 17, Last ann
CT580 hypothetical protein.
CPN0807 OR CPJ0807.
                                                                          MEDLINE=20330349; PubMed=10871362;
                                                                                                                                                                                                                                                                                     Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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InterPro; IPR003781; CoA_binding.
InterPro; IPR003781; CoA_binding.
InterPro; IPR00303; CoA_ligase.
Pfam; PF02629; CoA_binding; 1.
Pfam; PF02629; CoA_binding; 1.
Pfam; PF02649; ligase-CoA; 1.
TIGRPAMS; TIGR01019; succoAalpha; 1.
PROSITE; PS00399; SUCCINYL_COA_LIG_1; UNKNOWN_1.
                                                                                                  STRAIN=J138;
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QBYJE5;
QBYJE5;
QBYJE5;
Q1-MAR-2002 (TrEMBLre1. 20, Created)
Q1-MAR-2002 (TrEMBLre1. 20, Last sequence update)
Q1-JUN-2002 (TrEMBLre1. 21, Last annotation update)
Succinyl-CoA synthetase alpha chain (EC 6.2.1.5).
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Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
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MEDLINE=20020109; PubMed=11756688;
DelVecchio V.G. Kapatral V. Redkar R.J., Patra G., Mujer C., Los
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman
Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
Haselkorn R., Kyrpides N., Overbeek R.;
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E 300 AA; 31234
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100.0%; Pred. No.
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Last annotation update)
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RESULT 74
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Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey B.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weldman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Elsen J., Fraser C.M.;
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Q56567;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 11, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Vibrio anguillarum virC.
Vibrio anguillarum (Listonella anguillarum).
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Listonella.
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydo
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TIGR; CP1064; -.
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MEDLINE=96060845; PubMed=7590330;
Milton D.L., Norqvist A., Wolf-Watz H.;
"Sequence of a novel virulence-mediating gene, virC, anguillarum.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
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                                                                                                                                   SEQUENCE FROM N.A.
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nes 7; Conserv
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AP002548; BAA99015.1;
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X MEDILING=21470413; PubMed=11586360; A parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., A parkhill J., Wren B.W., Thomson N.R., Churcher C., Mungall K.L., A prentice M.B., Sebalhia M., James K.D., Churcher C., Mungall K.L., A prentice M.B., Sebalhia M., James K.D., Churcher C., Mungall K.L., A prentice M.B., Sebalhia M., James K.D., Erdeno-Tarraga A.M., A parker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., A parker S., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., A peltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., A Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Skelton J., Stevens K., Whitehead S., Barrell B.G.; X Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Nature 413:523-527(2001).

Nature 413:523-527(2001).

Nature 413:523-527(2001).

R EMBL; AJ414143; CAC893485.1; -.

R InterPro; IPR003662; sub_transporter.
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Best Local
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Best Local
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EMBL; U17054; AAA86984.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spiridonov N.A., Wong L., Johnson G.R.; "Homo sapiens CGI-55 protein mRNA."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q96SE2; PRELIMINARY;
Q96SE2;
Q1-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
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Mammalia; Eutheria;
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STRAIN=CO-92 / BIC
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01-JUN-2002
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01-MAR-2002
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                                                                                                                                                                                                                                                                                     Bacteria;
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                                                                                                                                                                                                                                                         TaxID=632;
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                                                                                                                                                                                                                                                                                     Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34888 MW;
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Primates;
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100.0%; Pred. No. 1.8e+02;
ive 0; Mismatches 0;
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Last annotation update)
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FBC15A2A76184429 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                           310 AA.
                                                                               the causative agent of plague.";
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RESULT 78
Q9EWZ9
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Best Local
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                                                                                                                            "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
    Oxidoreductase.
SROUENCE 312 AA;
                            InterPro; IPR002198; ADH short.
Pfam; PF00106; adh short; 1.
PRINTS; PR00080; SDEPAMILY.
PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
                                                                                          EMBL; AL445503; CAC13079.1; -. HSSP; P14061; 1FDU.
                                                                                                                                                                                                                                                                                                                                                            Redenbach M., Kieser H.M., Denapaite D., Eichner A., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicator A3(2) chromosome.",
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                       STRAIN=A3(2) / M145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A., Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97000351; PubMed=8843436;
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Submitted (OCT-2000) to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; St
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01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2002 (TrEMBLrel. 21,
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Pfam; PF03466; LysR_substrate; 1.
PRINTS; PR00039; HTHLYSR.
PROSITE; PS00217; SUGAR_TRANSPORT_2; UNKNOWN_1.
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                                                                                                                      (SDR) FAMILY.
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Pred. No. 1.9e+02;
C8AC48B96C0E5B73 CRC64;
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Matches 7
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Best Local
        "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
                                                  MEDLINE=21082930; PubMed=11214968; Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Tabata S.;
                                                                                                                                                                                                                                             01-OCT 2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-UTN-2002 (TrEMBLrel. 21, Last annotation update)
Permease protein of oligopeptide ABC transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Noelling J. Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.I., Sabathe F., Doucette-Stamm L., Soucaillé P., Daly M.J. Bennett G.N., Koonin E.V., Smith D.R.; "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetoburylicum."; "Bacteriol. 183:4823-4838(2001).

Bacteriol. 183:4823-4838(2001).

EMBL; ABO07761; AAK80582.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 315 AA; 36592 MW; 1188CD3EE3A22124 CRC64;
                                                                                                                                                                                                        Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q97FU1;
Q97FU1;
01-OCT-2001
01-OCT-2001
                                                                                                                                           STRAIN=MAFF303099;
                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                          Rhizobium loti (Mesorhizobium loti)
                                                                                                                                                                                                                                                                                                                 Q98IS2;
                                                                                                                                                                                  NCBI_TaxID=381;
                                                                                                                                                                                              Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                             Q98IS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
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Local Similarity 100.0%; P
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AP002999; BAB49444.1; -.
                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein CAC2635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.7%; Score 7;
100.0%; Pred. No.
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Pred. No.
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0. 1.9e+02;
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                                                                                                          Sasamoto S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P., Daly M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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RESULT 81
Q43055
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RESULT 82
Q91E43
ID Q91E4
AC Q91E4
AC Q91E4
DT 01-DE
DT 01-JU
DE US2 Phoci
OC Virus
OC Alpha
OX NCB1;
RN [1]
RN [1]
RR SEQUI
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Best Local S
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01-NOV-1996
01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Populus kitakamiensis (Aspen).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Roside
eurosids I; Malpighiales; Salicaceae; Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000515; BPD_transp.
Pfam; PF00528; BPD_transp; 1.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; UNKNOWN_1.
                                                                                                                                                                                                                                                     Q91E43; PRELIMINARY;
Q91E43; O1-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR002016; Peroxidase.
Pfam; PF00141; peroxidase; 1.
PRINTS; PR00458; PEROXIDASE.
PROSITE; PS00435; PEROXIDASE 1; 1.
PROSITE; PS00436; PEROXIDASE 2; 1.
Oxidoreductase; Peroxidase.
SEQUENCE 318 AA; 34172 MW; 14838148CD6076E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D11102; BAA01877.1; -. HSSP; P00433; 2ATJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Nucleotide sequence for the genomic DNA encoding an anionic peroxidase gene from a hybrid poplar, Populus kitakamiensis."; Biosci. Biotechnol. Biochem. 57:131-133(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kawai S., Matsumoto Y., Kajita
Morohoshi N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93169019; PubMed=7764045;
MEDLINE=93169019; PubMed=7764045;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peroxidase (EC 1.11.1.7).
                                                                                                                    viruses; dsuna viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
NCDT mair.
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  Martina B., Osterhaus A.D.M.E., Harder T.C.;
                           STRAIN-PB84;
                                                      SEQUENCE FROM N.A.
                                                                                                 NCBI_TaxID=47418;
                                                                                                                                                                                                                                     Us2 homologue (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            680 VILAGGP 686
                                                                                                                                                                                  Phocid herpesvirus 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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7; Conserv
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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100.0%; Pred. No.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                    325 AA.
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o. 1.9e+02;
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thes 0;
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                                                                                                                                                                                                                                                                update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               core eudicots; Rosidae;
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RA Salanoubat M., Lemcke K., Rieger M., Perez-Alonso M., Obermaier B.,
RA Partmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
RA Partmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
RA Perez M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Benes V.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Bargues M., Toppo S., Simionati B.,
RA Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsisk G.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Mannhaupt G., Haase D., Schoef H., Rudgus T., Vitale D.,
RA Mannhaupt G., Haase D., Schoef H., Rudgus T., Vitale D.,
RA Mayer K.F. X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Mayer X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Pai G., Miltscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Yokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.,
"Sequence and analysis of chromosome 3 of the plant Arabidopsis
"The Hallana", The Company M. Pallana B., Maraman M., Ca, Salada M., Tabata S.,
"Sequence and analysis of chromosome 3 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9CAX9
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Best Local
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification and analysis of immunogenicity of the glycoprotein D equivalentwithin the unique short segment of phocid herpesvirus-1."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ290955; CAC51462.1; -.

InterPro; IPR003485; Us2_Unk.
Pfam; PF02476; US2; 1.
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01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21016720; PubMed=11130713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                         EMBL; AC008153; AAG51446.1;
                                                                                Hypothetical
                                                                                                   Pfam; PF03492; Methytransf_6;
                                                                                                                      InterPro; IPR005299; Methytransf_6.
                                                                                                                                                          Nature 408:820-822(2000)
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7; Conserv
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                                                      protein.
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100.0%; Pred. No. 1.9
tive 0; Mismatches
                                                               37575 MW;
  0.7%;
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Score 7; I
Pred. No.
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                                                                 8B3FD25A11B8D700 CRC64;
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5. 1.9e+02;
      DB 10;
). 2e+02;
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                     Length 327;
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Q9PQG1
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                                                                                                                                                                                       STRAINATCC 824 / DSM 792 / VKM B-1787;
MEDLINE-21359325; PubMed=11466286;
Noelling J., Bretcon G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
J. Bacteriol. 181;4823-4838(2001).
EMBL, AE007594; AAK78764.1; -.
                                                                         InterPro; IPR000522; FecCD.
Pfam; PF01032; FecCD; 1.
ProDom; PD001557; FecCD; 1.
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01-JUN-2002
                                            Complete proteome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clostridium acetobutylicum.
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EMBL; AE002110; AAF30739.1; -.

Hypochetical protein; Complete

SEQUENCE 327 AA; 38114 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20500219; PubMed=11048724; Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen Cassell G.H.;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Mo
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01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein UU330.
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    336 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) (TrEMBLrel. 15, 0) (TrEMBLrel. 15, 12) (TrEMBLrel. 20, 12)
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(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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        36552 MW;
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; Pred. N
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Last annotation updat
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1BC0BC10C47B0F34 CRC64;
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321275386DAF61B7 CRC64;
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No. 2e+02;
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RESULT 87
Q8ZQT2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8ZQT2;
Q8ZQT2;
01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-UIN-2002 (TrEMBLrel. 21, Last annotation update)
3-deoxy-D-arabinohepulosonate-7-phosphate synthase
phenylalanine repressible) (EC 4.1.2.15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Delannoy E., Patil M., Essenberg M., Jalloul A., Marmey P., Daniel J.-F., Geiger J.-P., Nicole M.; "Gossypium hirsutum bacterial-induced peroxidase (podSSH1)."; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AF488305; AAL92037.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gossypium hirsutum (Upland cotton).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Malvales; Malvaceae; Gossypium.
EMBL; AB008731; AAL19699.1; ...
InterPro; IPR001785; DAHP_synth1.
Pfam; PF00793; DAHP_synth1; 1.
ProDom; PD005060; DAHP_synth1; 1.
                                                                                                                                                                                                                                                McClelland M., Sanderson K.E., Spieth J., Clifton S.W. Courtney L., Porwollik S., Ali J., Dante M., Du F., HoLeonard S., Nguyen C., Scott K., Holmes A., Grewal N.,
                                                                                                                                                                                                                                                                                                                                 STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
                                                                                                                 Nature 413:852-856(2001).
                                                                                                                                                                                                  Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella typhimurium.
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SECUENCE 347 AA; 37407 MW;
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Bacterial-induced peroxidase (EC 1.11.1.7).
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                                                                                                                                                                  "Complete genome sequence of Salmonella enterica serovar Typhimurium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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nes 7; Conserv
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o. 2e+02;
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Hou S., Layman D.
N., Mulvaney E.,
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Best Local :
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Best Local Similarity
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"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413:888-852(2001).
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Phospho-2-dehydro-3-deoxyheptonate aldolase (DAHP s
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STY0801.
                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Hypothetical protein ECU07_1170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 350 AA;
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Pfam; PF00793; DAHP_synth1; 1.
ProDom; PD005060; DAHP_synth1; 1.
TIGRPAMs; TIGR00034; aTOFGH; 1.
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SEQUENCE FROM N.A.
                                                                         Encephalitozoon cuniculi.
Eukaryota; Microsporidia;
                                                                                                                                                                                                                                                                                              TANS8Ö
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                                          NCBI_TaxID=6035;
                                                                                                                                  ECU07_1170.
                                                                                                                                                                                                                                                                       (1XNS8D
                                                                                                                                                                                                                                                                                                                                                                                                                                    141 AGEFLDM 147
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                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37868 MW; C764207BBAB65FB7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.7%; Score 7;
100.0%; Pred. No.
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                                                                            Unikaryonidae;
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                                                                                                                                                                                                               sequence update)
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                                                                                                                                                                                                                                                                                              357 AA
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o. 2.1e+02;
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). 2.1e+02;
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                                                                            Encephalitozoon
                                                                                                                                                                                     update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 350;
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SO DE RELEGIO
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Best Local
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                     Q9CN76;
Q9CN76;
01-JUN-2001
01-JUN-2001
01-JUN-2002
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Q92HR6;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=GB-M1;
MEDLINB=21576510; PubMed=11719806;
MEDLINB=21576510; PubMed=11719806;
Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P.
Pelbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
Weissenbach J., Vivares C.P.;
Weissenbach J., Vivares C.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to microcin C7 self-immunity protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Encephalitozoon cuniculi.";
Nature 414:450-453(2001).
EMBL; AL590447; CAD25650.1; -.
                                                                                                                                                                                                                                                                                Science 293:2093-2098(2001).
EMBL; AE008629; AAL03243.1; -.
InterPro; IPR003507; UPF0094.
                                                                                                                                                                                                                                                                                                                                                MEDLINE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=MALISH 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similar to microcin MCCF2 OR RC0705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted [2]
                                                                                                                                                                                                                                           SEQUENCE 360 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rickettsia conorii.
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AROG OR PM0563.
                                                                                                                                                                                                                                                                       Pfam; PF02016; UPF0094; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=781
                                                                                                                                                                                                                                                                                                                                     Raoult D.;
                                                                                                                                                                                                                                                                                                                       Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 NTPTRTF 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 663 NTPTRTF 669
                                                                                                                                                                 874 GIQKTTY 880
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                                                                                                                                                                                           Local Similarity
                                                                                                                                        5 GIOKTTY 11
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                       (TrEMBLrel. 17, (TrEMBLrel. 17, (TrEMBLrel. 21,
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Conservative 0; Mismatches
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                                                                          PRELIMINARY;
                                                                                                                                                                                       100.0%;
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                                                                                                                                                                                                                                              40394 MW;
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                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                           Score 7; DB 16; L
Pred. No. 2.1e+02;
0; Mismatches 0;
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RESULT 92
Q95KA0
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        BARARE
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Best Local (
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Best Local
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 39.3 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB063042; BAB60776.1; -. InterPro; IPR000873; AMP-bind. Ffam; PF00501; AMP-binding; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-MEDULLA OBLOGATA;
Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M.,
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 361 AA;
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Pfam; PF00793; DAHP_synth1; 1.
ProDom; PD005060; DAHP_synth1; 1.
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                                                                                Q9FC16;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein. SEQUENCE 364 AA; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   libraries.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                            01-MAR-2001
01-JUN-2002
                                                                                                                                          Q9FCI6
                                                                                                                                                                                                                                                                              350
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                                                                                                                                                                                                                                                                                                                                  412 PAGTEPA 418
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7; Conserv
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                       I (TrEMBLrel. 16,
I (TrEMBLrel. 16,
2 (TrEMBLrel. 21,
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protein.
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100.0%; Pred. No
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                         Last sequence update)
Last annotation update)
                                                                                Created)
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Pred. No.
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Mismatches
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o. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                               DB 6; Ler
o. 2.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 364;
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P91984;
01-MAY-1997 (TrEMBLrel. 03,
01-MAY-1997 (TrEMBLrel. 03,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M. Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S. Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rurberford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K. Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                             Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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Streptomyces coelicolor.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                               C50B6.10 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL39098; CAC01332.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hopwood D.A.; "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=A3(2) / M145;
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MEDLINE=99069613; PubMed=9851916;
                      SEQUENCE FROM N.A.
                                                                Submitted (OCT-1996)
                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                  NCBI_TaxID=6239;
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SM00228; PDZ; 1.
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the EMBL/GenBank/DDBJ databases.
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o. 2.1e+02;
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Q9CRR7
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Q9CBV6
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Science 282:2012-2018(1998).
EMBL; Z81050; CAB02859.1; -.
InterPro; IPR003002; 7TM chemo1.
InterPro; IPR000168; 7TM nematode.
Pfam; PF01461; 7tm 4; 1.
SEQUENCE 371 AA; 42447 MM; 872EE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-11, MEDLINE-21, PubMed=11234002;
MEDLINE-1128732; PubMed=11234002;
MEDLINE-1128732; PubMed=11234002;
Medeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Mungall K., Basham D., Brown D., Chillingworth T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quall M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS; TIGR00518; alaDH; 1.

PROSITE; PS00836; ALADH PNT 1; 1.

PROSITE; PS00837; ALADH PNT 2; 1.

PAD; Flavoprotein; Oxidoreductase; Complete proteome.

PAD; Flavoprotein; Oxidoreductase; Complete proteome.

SEQUENCE 371 AA; 38845 MW; 35425DE604EF8199 CRC64;
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HSSP; Q60164; 1HZZ.
Leproma; ML1532; -.
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01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR004002; AlaDh_PNT:
InterPro; IPR001327; FAD_Dyr_redox.
InterPro; IPR000205; NAD_binding.
Pfam; PF01262; AlaDh_PNT; 1.
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Barrell B.G.;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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"Genome sequence of the nematode C.elegans: A platform
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les 7; Conserv
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No. 2.2e+02;
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RESULT 97
Q91WP3
ID Q91WI
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DT 01-D;
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                                                                                                                         Q91WP3 PRELIMINARY; PRT; 386 AA.
Q91WP3;
Q91WP3;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Q9CRR7;
01-JUN-2001
01-JUN-2001
                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00523; DWA; 1.
SMART; SM00524; DWB; 1.
NON_TER 377 377
                                                                                   Mus musculus (Mouse)
                                                                                                                Similar to RIKEN cDNA 1200009K13 gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF03165; MH1; 1. Pfam; PF03166; MH2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 FHSVELN 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 409:685-690(2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    łayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                      FHSVELN
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IPR003619; Dwarfin_A.
IPR004863; MH1.
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Rodentia;
                                  Rodentia;
                                                         Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42204 MW; 830E5E1452D025DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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100.0%; Pred. No.
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                               Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
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o. 2.2e+02;
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                                  Murinae;
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RESULT 99
Q9Y4S3
ID Q9Y4S
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L. Belchi w. Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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  Q9Y4S3
                                                                                                                                                                                                                                                                                                                                                                Hypothetical SEQUENCE 38
                                                                                                                                                                                                                                                                                                                                                                                                                  TubercuList; Rv3680; -..
InterPro; IPR003348; ArsA_ATPase.
Pfam; PF02374; ArsA_ATPase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                           24 RLWRLLL 30
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                                                                                                                                         RLWRLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL022121; CAA18002.1; AE007175; AAK48149.1;
                                                                                                                                                                                                                                                Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                             386 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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  PRELIMINARY;
                                                                                                                                         184
                                                                                                                                                                                                                                                                                                                                                             protein; Complete proteome.
36 AA; 41404 MW; AB6D2D31A44620B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OSHKOSH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13665:1; *.
42235 MW; A22FB50BE68F72CB CRC64;
                                                                                                                                                                                                                                          100.0%; +1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.7%; Score 7; 1
100.0%; Pred. No.
                                                                                                                                                                                                                                                   0.7%; Score 7; DB 1100.0%; Pred. No. 2.1 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
ATPase (Hypothetical pr
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                                                                                                                                                                                                                                          DB 16; L., NO. 2.3e+02; 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          386
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o. 2.3e+02;
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                                                                                                                                                                                                                                                                                                        Length 386;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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RA Alvarenga R., Alves L.M.C., Arvuda P., Abreu F.A., Acencio M., Raylavarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S., Raylavarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S., Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Raylavarenga M.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Costa M.C., Costa M.C.R., Costa-Neto C.M., Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., Racincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Racincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Raylavarenga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., Raylavarenga J.S., Kuramae S.C., Franco M.H.S., Gomes S.L., Gruber A., Raylavarenga M.D., Junqueira M.L., Kemper E.L., Kitajima J.P., Raylavarenga M.D., Leite L.C.C., Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A., Marchado M.A., Madeira A.M.B.N., Madeira H.M.F., Matsukuma A.Y., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., Marmock C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MILITED (NOV-2001) to the EMB. 2 EMBL; ALO80119; CAB45718.1; -. EMBL; BC017449; AAH17449.1; -- Hypothetical protein. SEQUENCE 387 **
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 42.4 kDa protein (PAI-1 mRNA-binding protein).
EXERCISE (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21154917; PubMed=11230166; Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S. Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., Lauber J., Ottenwaelder B., Obermaier B., Tampe J., Heubner D. Mewes H.W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D. Mewes H.W., Körn B., Klein M., Poustka A.; "Towards a Catalog of Human Genes and Proteins: Sequencing and Analysis of 500 Novel Complete Protein Coding Human cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9PCI2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9Y4S3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=LUNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 11:422-435(2001).
                                                                                                                                                                                                                                                                                               MEDLINE=20365717; PubMed=10910347;
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Xylella fastidiosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Porphyrin biosynthesis protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247
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                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           487 ADTENKE 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADTENKE 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42426 MW; 8C47134D22C1CCFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.7%; Score 7;
[00.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                   gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         389
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RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Mani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA de Souza A.P., Terenzi M.E., Truffi D., Teai S.M., Tsuhako M.H.,
RA de Souza A.P., Terenzi M.E., Truffi D., Teai S.M., Tsuhako M.H.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RI Mature 406:15:1-159(2000).
DR EMBL; AE004001; AAF84605.1; -.
DR InterPro; IPROU1440; TPR.
Complete proteome.
SQ SEQUENCE 389 AA; 44436 MW; 24597773D3632925 CRC64;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 181 LPPRGLL 187

Search completed: April 22, 2003, 15:35:32

Job time: 72 secs
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